



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Chatterjee, Malaya
Foon, Kenneth A.
Chatterjee, Sunil K.
- (ii) TITLE OF INVENTION: MURINE MONOCLONAL ANTI-IDIOTYPE ANTIBODY
11D10 AND METHODS OF USE THEREOF
- (iii) NUMBER OF SEQUENCES: 59
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: MORRISON & FOERSTER
 - (B) STREET: 755 PAGE MILL ROAD
 - (C) CITY: PALO ALTO
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94304-1018
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/766,350
 - (B) FILING DATE: 13-DEC-1996
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Polizzi, Catherine M.
 - (B) REGISTRATION NUMBER: 40,130
 - (C) REFERENCE/DOCKET NUMBER: 30414-20003.21
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 - (C) TELEX: 706141

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 435 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..435

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GGG GCC CCT GCT CAG ATT CTT GGG TTC TTG TTG CTC TTG TTT CCA 48
Met Gly Ala Pro Ala Gln Ile Leu Gly Phe Leu Leu Leu Phe Pro
-20 -15 -10 -5

GGT ACC AGA TGT GAC ATC CAG ATG ACC CAG TCT CCA TCC TCC TTA TCT 96
Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
1 5 10

GCC TCT CTG GGA CAA AGA GTC AGT CTC ACT TGT CGG GCA AGT CAG GAC 144
Ala Ser Leu Gly Gln Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp
15 20 25

ATT GGT ATT AAC TTA CAT TGG CTT CAG CAG GAA CCA GAT GGA ACT ATT 192
Ile Gly Ile Asn Leu His Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile
30 35 40

AAA CGC CTG ATC TAC GCC ACA TCC AGT TTA GGT TCT GGT GTC CCC AAA 240
Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Gly Ser Gly Val Pro Lys
45 50 55 60

AGG TTC AGT GGC AGT AGG TCT GGG TCA GAT TAT TCT CTC ACC ATC AGC 288
Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser
65 70 75

AGC CTT GAG TCT GAA GAT TTT GTA GCC TAT TAC TGT CTA CAA TAT GCT 336
Ser Leu Glu Ser Glu Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala
80 85 90

AGT TCT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA CGG 384
Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
95 100 105

GCT GAT GCT GCA CCA ACT GTA TCC ATC TTC CCA CCA TCC AGT AAG CTT 432
Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Lys Leu
110 115 120

GGG 435
Gly
125

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Ala Pro Ala Gln Ile Leu Gly Phe Leu Leu Leu Leu Phe Pro
-20 -15 -10 -5
Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
1 5 10
Ala Ser Leu Gly Gln Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp
15 20 25
Ile Gly Ile Asn Leu His Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile
30 35 40
Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Gly Ser Gly Val Pro Lys
45 50 55 60
Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser
65 70 75
Ser Leu Glu Ser Glu Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala
80 85 90
Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
95 100 105
Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Lys Leu
110 115 120
Gly
125

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..459

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 58

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG GAA TGC AGC TGG GTC TTT CTC TTC CTC CTG TCA ATA ACT ACA GGT 48
Met Glu Cys Ser Trp Val Phe Leu Phe Leu Leu Ser Ile Thr Thr Gly
-19 -15 -10 -5

GTC CAC TCC CAG GCT TAT CTA CAG CAG TCT GGG GCT GAG CTG GTG AGG 96
Val His Ser Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
1 5 10

TCT GGG GCC TCA GTG AAG ATG TCC TGC AAG GCT TCT GGC TAC ACA TTG 144
Ser Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Leu
15 20 25

ACC AGT TAC AAT ATG CAC TGG GTA AAG CAG ACA CCT GGA CAG GGC CTG 192
Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu
30 35 40 45

GAA TGG ATT GGA AAT ATT TTT CCT GGA AAT GGT GAT ACT TAC TAC AAT 240
Glu Trp Ile Gly Asn Ile Phe Pro Gly Asn Gly Asp Thr Tyr Tyr Asn
50 55 60

CAG AAG TTT AAG GGC AAG GCC TCA TTG ACT GCA GAC ACA TCC TCC AGC 288
Gln Lys Phe Lys Gly Lys Ala Ser Leu Thr Ala Asp Thr Ser Ser Ser
65 70 75

ACA GCC TAC ATG CAG ATC AGC AGC CTG ACA TCT GAA GAC TCT GCG GTC 336
Thr Ala Tyr Met Gln Ile Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
80 85 90

TAT TTC TGT GCA AGA GGG AAC TGG GAG GGT GCT CTG GAC TAC TGG GGT 384
Tyr Phe Cys Ala Arg Gly Asn Trp Glu Gly Ala Leu Asp Tyr Trp Gly
95 100 105

CAA GGA ACC TCA GTC ACC GTC TCC TCA GCC AAA ACG ACA CCC CCA CCC 432
Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Pro
110 115 120 125

GTC TAT CCA CTG GTC CCT GGA AGC TTG GG 461
Val Tyr Pro Leu Val Pro Gly Ser Leu
130

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Glu Cys Ser Trp Val Phe Leu Phe Leu Leu Ser Ile Thr Thr Gly
-19 -15 -10 -5

Val His Ser Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
 1 5 10
 Ser Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Leu
 15 20 25
 Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu
 30 35 40 45
 Glu Trp Ile Gly Asn Ile Phe Pro Gly Asn Gly Asp Thr Tyr Tyr Asn
 50 55 60
 Gln Lys Phe Lys Gly Lys Ala Ser Leu Thr Ala Asp Thr Ser Ser Ser
 65 70 75
 Thr Ala Tyr Met Gln Ile Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
 80 85 90
 Tyr Phe Cys Ala Arg Gly Asn Trp Glu Gly Ala Leu Asp Tyr Trp Gly
 95 100 105
 Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Pro
 110 115 120 125
 Val Tyr Pro Leu Val Pro Gly Ser Leu
 130

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT	60
CTCACTTGTC GGGCAAGTCA GGACATTGGT AGTAGCTTAA ACTGGCTTCA GCAGGAACCA	120
GATGGAACTA TTAAACGCCT GATCTACGCC ACATCCAGTT TAGATTCTGG TGTGCCCAAA	180
AGGTTTCAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT	240
GAAGATTTTG TAGACTATTA CTGTCTACAA TATGCTAGTT CTCCGTACAC GTTCGGAGGG	300
GGGACCAAGC TGGAAATAAA A	321

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GANATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT 60
CTCACTTGTC GGGCAAGTCA GGACATTGGT AGTAGCTTAA ACTGGCTTCA GCAGGAACCA 120
GATGGAACCTT TTAAACGCCT GATCTACGCC ACATCCAGTT TAGATTCTGG TGTCCCCAAA 180
AGGTTTCAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT 240
GAAGATTTTG TAGACTATTA CTGTCTACAA TATGCTAGTT GTCCGTACAC GTTCGGAGGG 300
GGGACCAAGC TGGAAATAAA A 321

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT 60
CTCACTTGTC GGGCAAGTCA GGACATTGGT AGTAGCTTAA ACTGGCTTCA GCAGGAACCA 120
GATGGAACCTA TTAAACGCCT GATCTACGCC ACATCCAGTT TAGATTCTGG TGTCCCCAAA 180
AGGTTTCAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT 240
GAAGATTTTG TAGACTATTA CTGTCTACAA TATGCTAGTT CTCCGTGGAC GTTCGGTGGA 300
GGCACCAAGC TGGAAATCAA A 321

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT 60
CTCACTTGTC GGCCAAGTCA GGACATTGGT AGTAGCTTAA ACTGGCTTCA GCAGGAACCA 120
GATGGAACCTA TTAAACGCCT GATCTACGCC ACATCCAGTT TAGATTCTGG TGTCCCCAAA 180
AGGTTTCAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT 240

GAAGATTTTG TAGACTATTA CTGTCTACAA TATGCTAGTT CTCCGTGGAC GTTCGGTGGA 300
GGCACCAAGC TGGAAATCAA A 321

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 321 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT 60
CTCACTTGTC GGCCAAGTCA GGACATTGGT AGTAGCTTAA ACTGGCTTCA GCAGGAACCA 120
GATGGAATA TTAAACGCCT GATCTACGCC ACATCCAGTT TAGATTCTGG TGTCCCCAAA 180
AGGTTCACTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT 240
GAAGATTTTG TAGACTATTA CTGTCTACAA TATGCTAGTT CTCCGTGGAC GTTCGGTGGA 300
GGCACCAAGC TGGAAATCAA A 321

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATCCAGATGA CCCAGTCTCC ATCCTCCTTA TCTGCCTCTC TGGGAGAAAG AGTCAGTCTC 60
ACTTGTCTGG CAAGTCAGGA CATTGGTAGT AGCTTAAACT GGCTTCAGCA GGAACCAGAC 120
GGAATAATTA AACGCCTGAT CTACGCCACA TCCAGTTTAG ATTCTGGTGT CCCCCAAAGG 180
TTCAGTGGCA GTAGGTCTGG GTCAGATTAT TCTCTACCA TCAGCAGCCT TGAGTCTGAA 240
GATTTTGTAG ACTATTACTG TCTACAATAT GCTAGTTCTC CGTGGACGTT CGGTGGAGGC 300
ACCAAGCTGG AAATCAAA 318

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 303 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TCTCCATCCT CCTTATCTGC CTCTCTGGGA GAAAGAGTCA GTCTCACTTG TCGGGCAAGT 60
CAGGACATTG GTAGTAGCTT AAAGTGGCTT CAGCAGGAAC CAGATGGAAC TATTAAACGC 120
CTGATCTACG CCACATCCAG TTTAGATTCT GGTGTCCCCA AAAGGTTTCA TGGCAGTAGG 180
TCTGGGTCAG ATTATTCTCT CACCATCAGC AGCCTTGAGT CTGAAGATTT TGTAGACTAT 240
TACTGTCTAC AATATGCTAG TTCTCCGTAC ACGTTCGGAG GGGGGACCAA GCTGNAAATA 300
AAA 303

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT 60
CTCACTTGTC GGGCAAGTCA GGAAATTAGT GGTTACTTAA GCTGGCTTCA GCAGAAACCA 120
GATGGAAC TAACACGCCT GATCTACAGC ACATCCACTT TAAATTCTGG TGTCCCAAAA 180
AGGTTCAAGT GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT 240
GAAGATTTTG CAGACTATTA CTGTCTACAA TATGCTAGTT CTCCGTACAC GTTCGGAGGG 300
GGGACCAAAC TGGAATAAAA A 321

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TCTCCATCCT CCTTATCTGC CTCTCTGGGA GAAAGAGTCA GTCTCACTTG TCGGGCAAGT 60
CAGGACATTG GTAATAGCTT AAAGTGGCTT CAGCAGGAAC CAGATGGAAC TATTAAACGC 120
CTGATCTACG CCACATCCAG TTTAGATTCT GGTGTCCCCA AAAGGTTTCA TGGCAGTAGG 180

TCTGGGTCAG ATTATTCTCT CACCATCAGC AGCCTTGAAT CTGAAGATTT TGTAGTCTAT 240
TACTGTCTAC AATATGCTAG TTATACGTAC ACGTTCGGAG GGGGGACCAA GTTGGAAC TA 300
AAA 303

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT 60
CTCACTTGTC GGGCAAGTCA GGAAATTAGT GGT TACTTAA GCTGGCTTCA GCAGAAACCA 120
GATGGAAC TA TTAAACGCCT GATCTACGCC GCATCCACTT TAGATTCTGG TGTCCCAAAA 180
AGGTT CAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT 240
GAAGATTTTG CAGACTATTA CTGTCTACAA TATCTTAGTT ATCCGCTCAC GTTCGGTGCT 300
GGGACCAAGC TGGAGCTGAA A 321

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 294 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CAGGCTTATN TACAGCAGTC TGGGGCTGAG CTGGTGAGGC CTGGGGCCTC AGTGAAGATG 60
TCCTGCAAGG CTTCTGGCTA CACATTTACC AGTTACAATA TGCACTGGGT AAAGCAGACA 120
CCTAGACAGG GCCTGGAATG GATTGGAGCT ATTTATCCAG GAAATGGTGA TACTTCCTAC 180
AATCAGAAGT TCAAGGGCAA GGCCACACTG ACTGTAGACA AATCCTCCAG CACAGCCTAC 240
ATGCAGCTCA GCAGCCTGAC ATCTGAAGAC TCTGCGGTCT ATTTCTGTGC AAGA 294

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TGCTATGGAC TACTGGGGTC AAGGAACCTC AGTCACCGTC TCCTCA 46

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CAGGCTTATG TACAGCAGTC TGGGGCTGAG CTGGTGAGGC CTGGGGCCTC AGTGAAGATG 60
TCCTGCAAGG CTTCTGGCTA CAGATTTACC AGTTACAATA TGCACTGGGT AAAGCAGACA 120
CGTAGACAGG GCCTGGAATG GATTGGAGCA ATTTATCCAG GAAATGGTGA TACTTCCTAT 180
AATCAGAAGT TCAAGGGCAA GGCCACACTG ATTGTAGACA AATCCTCCAG CACAGCCTAC 240
ATGCAGCTCA GCAGCCTGAC ATCTGAAGAC TCTGCGGTCT ATTTCTGTGC AAGAGAGAGG 300
GGTAACTACG TAGGACATAT GGACTACTGG GGTCAAGGAA CCTCAGTCAC CGTCTCCTCA 360

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CAGGCTTATC TACAGCAGTC TGGGGCTGAG CTGGTAAGGC CTGGGTCCTC AGTGAAGATG 60
TCCTGCAAGG CTTCTGGCTA CACATTTACC AGTTACAATA TGCACTGGGT AAAGCAGACA 120
CCTAGACAGG GCCTGGAATG GATTGGAGCT ATTTATCCAG GAAATGGTGA TACTTCCTAC 180
AATCAGAAGT TCAAGGGCAA GGCCACACTG ACTGTAGACA AATCCTCCAG CACAGCCTAC 240
ATGCAGCTCA GCAGCCTGAC ATCTGAAGAC TCTGCGGTCT ATTTCTGTGC AAGAGGGGAT 300
TACTCCGGTA GTATAGACTA CTGGGGCCAA GGCACCACTC TCACAGTCTC CTCA 354

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 297 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAGGCTTATC TACAGCAGTC TGGGGCTGAG CTGGTGAGGC CTGGGGCCTC AGTGAAGATG 60
TCCTGCAAGG CTTCTGGCTA CACATTTACC AGTTACAATA TGCACTGGGT AAAGCAGACA 120
CCTAGACAGG GCCTGGAATG GATTGGAGCT ATTTATCCAG GAAATGGTGA TACTTCCTAC 180
AATCAGAAGT TCAAGGGCAA GGCCACACTG ACTGTAGACA AATCCTCCAG CACAGCCTAC 240
ATGCAGCTCA GCAGCCTGAC ATCTGAAGAC TCTGCGGTCT ATTTCTGTGC AAGAGTG 297

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CTGGGGCACA GGGACCACGG TCACCGTCTC C 31

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 297 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CAGGCTTATC TACAGCAGTC TGGGGCTGAG CTGGTGAGGC CTGGGGCCTC AGTGAAGATG 60
TCCTGCAAGG CTTCTGGCTA CACATTTACC AGTTACAATA TGCACTGGGT AAAGCAGACA 120
CCTAGACAGG GCCTGGAATG GATTGGAGCT ATTTATCCAG GAAATGGTGA TACTTCCTAC 180
AATCAGAAGT TCAAGGGCAA GGCCACACTG ACTGTAGACA AATCCTCCAG CACAGCCTAC 240
ATGCAGCTCA GCAGCCTGAC ATCTGAAGAC TCTGCGGTCT ATTTCTGTGC AAGAGTG 297

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTGGGGCACA GGGACCACGG TCACCGTCTC 30

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AGGTCCAGCT GCAGCAGTCT GGACCTGAGC TGGTAAAGCC TGGGGCTTCA GTGAAGATAT 60
CCTGCAAGGC TTCTGGATAC ACATTCCTG ACTACTACAT GCACTGGGTG AAGCAGAAGC 120
CTGGGCAGGG CCTTGAGTGG ATTGGAGAGA TTTATCCTGG AAGTGTAAT ACTTACTACA 180
ATGAGAAGTT CAAGGGYAAG GCCTCACTGA CTGCAGACAA ATCCTCCAGC ACAGCCTACA 240
TGCAGCTCAG CAGCCTGACA TCTGAGGACT CTGCAGTCTA TTTCTGTGCA AGACGTTACT 300

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TGCTATGGAC TACTGGGGTC AAGGAACCTC AGTCACCGTC TCCTCA 46

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CAGGTTTCAGC TCCAGCAGTC TGGGGCTGAG CTGGCAAGAC CTGGGGCTTC AGTGAAGTTG	60
TCCTGCAAGG CTTCTGGCTA CACCTTTACT AGCTACTGGA TGCAGTGGGT AAAACAGAGG	120
CCTGGACAGG GTCTGGAATG GATTGGGGCT ATTTATCCTG GAGATGGTGA TACTAGGTAC	180
ACTCAGAAGT TCAAGGGCAA GGCCACATTG ACTGCAGATA AATCCTCCAG CACAGCCTAC	240
ATGCAACTCA GCAGCTTGGC ATCTGAGGAC TCTGCGGTCT ATTACTGTGC AAGAG	295

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGCTATGGAC TACTGGGGTC AAGGAACCTC AGTCACCGTC TCCTCA	46
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(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CAGGTTTCAGC TCCAGCAGTC TGGGGCTGAG CTGGCAAGAC CTGGGGCTTC AGTGAAGTTG	60
TCCTGCAAGG CTTCTGGCTA CACCTTTACT AGCTACTGGA TGCAGTGGGT AAAACAGAGG	120
CCTGGACAGG GTCTGGAATG GATTGGGGCT ATTTATCCTG GAGATGGTGA TACTAGGTAC	180
ACTCAGAAGT TCAAGGGCAA GGCCACATTG ACTGCAGATA AATCCTCCAG CACAGCCTAC	240
ATGCAACTCA GCAGCTTGGC ATCTGAGGAC TCTGCGGTCT ATTACTGTGC AAGA	294

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TGCTATGGAC TACTGGGGTC AAGGAACCTC AGTCACCGTC TCCTCA

46

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAGGTTTCAGC TCCAGCAGTC TGGGGCTGAG CTGGCAAGAC CTGGGGCTTC AGTGAAGTTG 60

TCCTGCAAGG CTTCTGGCTA CACCTTTACT AGCTACTGGA TGCAGTGGGT AAAACAGAGG 120

CCTGGACAGG GTCTGGAATG GATTGGGGCT ATTTATCCTG GAGATGGTGA TACTAGGTAC 180

ACTCAGAAGT TCAAGGGCAA GGCCACATTG ACTGCAGATA AATCCTCCAG CACAGCCTAC 240

ATGCAACTCA GCAGCTTGGC ATCTGAGGAC TCTGCGGTCT ATTACTGTGC AAGA 294

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TGCTATGGAC TACTGGGGTC AAGGAACCTC AGTCACCGTC TCCTCA

46

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CAGGTCCAAC TGCAGCAGCC TGGTGCTGAG CTTGTGAAGC CTGGGGCCTC AGTGAAGCTG 60

TCCTGCAAGG CTTCTGGCTA CACTTTCACC AGCTACTGGA TAAACTGGGT GAAGCAGAGG 120

CCTGGACAAG GCCTTGAGTG GATTGGAAAT ATTTATCCTG GTAGTAGTAG TACTAACTAC 180

AATGAGAAGT TCAAGAGCAA GGCCCACTG ACTGTAGACA CATCCTCCAG CACAGCCTAC 240

ATGCAGCTCA GCAGCCTGAC ATCTGACGAC TCTGCGGTCT ATTATTGTGC AAGACG

296

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TGCTATGGAC TACTGGGGTC AAGGAACCTC AGTCACCGTC TCCTCA

46

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 9
(D) OTHER INFORMATION: /note= "May also be the amino acid arginine(R) "

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 15
(D) OTHER INFORMATION: /note= "May also be the amino acid glutamine(E) "

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 16
(D) OTHER INFORMATION: /note= "May also be the amino acid serine(S) "

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 19
(D) OTHER INFORMATION: /note= "May also be the amino acid proline(P) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
1 5 10 15

Arg Pro Ala Pro
20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /note= "May also be the amino acid arginine(R)"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /note= "May also be the amino acid glutamine(E)"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 19
- (D) OTHER INFORMATION: /note= "May also be the amino acid serine(S)"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 22
- (D) OTHER INFORMATION: /note= "May also be the amino acid proline(P)"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "May also be the amino acid proline(P)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala
1 5 10 15

Pro Asp Thr Arg Pro Ala Pro
 20

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: misc_difference

(B) LOCATION: replace(30, "")

(D) OTHER INFORMATION: /note= "N represents the nucleotide
Inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CCCAAGCTTC CAGGGRCCAR KGGATARACN GRTGG

35

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGGAATTCAT GRAATGSASC TGGGTyWtyC TCTT

34

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TAATACGACT CACTATAGGG

20

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GTTTTCCCAG TCACGACGT

19

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ACTAGTCGAC ATGAGGRCCC CTGCTCAGWT TYTTGGNWTCTT

42

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCCAAGCTTA CTGGATGGTG GGAAGATGGA

30

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CAGATGGAAG GGCCCAAC

18

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GATTGATGCA TATCATTACC

20

(2) INFORMATION FOR SEQ ID NO:44:


- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GTTATCGATG TCGAATAGCC

20

(2) INFORMATION FOR SEQ ID NO:45:

- 
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TTGCTGCAGA TTGAGTACTG TTCT

24

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15
Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp Ile Gly Ser Ser
20 25 30
Leu Asn Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile Lys Arg Leu Ile
35 40 45
Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly
50 55 60
Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
65 70 75 80
Gly Asp Phe Val Asp Tyr Tyr Cys Leu Gln Tyr Ala Ser Ser Pro Tyr
85 90 95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
1 5 10 15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30
Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Asn Tyr Asn Gln Lys Phe
50 55 60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95
Ala Arg Gly Xaa Xaa Xaa Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr
100 105 110
Ser Val Thr Val Ser Ser
115

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear


(ix) FEATURE:

- (A) NAME/KEY: Region
 (B) LOCATION: 1..4
 (D) OTHER INFORMATION: /note= "position 54-57 of 11D10
comparison sequence #8 (Fig. 26B)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Ser Asp Ser Tyr
1

(2) INFORMATION FOR SEQ ID NO:50:

- 
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Region
 (B) LOCATION: 1..9
 (D) OTHER INFORMATION: /note= "positions 118-126 of 11d10
comparison sequence #2 and positions 100-108 of 11d10 comparison
sequence #6 (Fig. 26B)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: Region
 (B) LOCATION: 1..7
 (D) OTHER INFORMATION: /note= "positions 99-105 of 11D10
comparison sequence #3 and #8 (Fig. 26B)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: Region
 (B) LOCATION: 1..4
 (D) OTHER INFORMATION: /note= "positions 100-103 of 11D10
comparison sequence #12 (Fig. 26B)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Val Tyr Tyr Tyr
1

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: Region
 (B) LOCATION: 1..4
 (D) OTHER INFORMATION: /note= "positions 100-103 of 11D10
comparison sequence #14 (Fig. 26B)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Phe Tyr Phe Tyr
1

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ix) FEATURE:
 (A) NAME/KEY: Region
 (B) LOCATION: 1..4
 (D) OTHER INFORMATION: /note= "positions 100-103 of 11D10
comparison sequence #15(Fig. 26B)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Gly Leu Phe Thr
1

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Gly Ser Thr Ala Pro Pro Ala His Arg Val Thr Ser Ala Pro Glu Ser
1 5 10 15
Arg Pro Pro Pro
20

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Pro Pro Pro Arg Ser Glu Pro Ala Ser Thr Val Arg His Ala Pro Pro
1 5 10 15
Ala Thr Ser Gly
20

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Ala Pro Asp Thr Arg Pro Pro Pro
1 5

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Met Gly Thr Pro Ala Gln Ile Leu Gly Phe Leu Leu Leu Leu Phe Pro
1 5 10 15

Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

Ala Ser Leu Gly Gln Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp
35 40 45

Ile Gly Ile Asn Leu His Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile
50 55 60

Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Gly Ser Gly Val Pro Lys
65 70 75 80

Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser
85 90 95

Ser Leu Glu Ser Gly Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala
100 105 110

Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
115 120 125

Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Lys Leu
130 135 140

Gly
145

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ix) FEATURE:
 (A) NAME/KEY: Region
 (B) LOCATION: 1..4
 (D) OTHER INFORMATION: /note= "position 2-5 of 11D10
comparison sequence #15 (Fig. 26A)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Glu Leu Val Leu
1

A1